

09/068372

FIL 1A

PSTPIP 1 MMAQLQFRDAFWCRDF - - TAHTGYEVLLQRLLDGRKMCKDVEELLRQRAQ
cdc15 1 - - - - - MLTKSLOGSEDA GMDALMSRTKSSLSVLESIDEFYAKRAS

*
PSTPIP 49 A E E R Y G K E L V Q I A R K A G G Q T E M N S L R T S F D S L K Q Q T E N V G S A H I Q L A L A L
cdc15 41 I E R E Y A S K L Q E L A A S S A D I P E V G S T L N N I L S M R T E T G S M A K A H E E V S Q Q I

PSTPIP 99 R E E L R S - L E E F R E R Q K E Q R K K Y E A I M D R V Q K S K L S L Y K K T M E S K K A Y D Q K
cdc15 91 N T E L R N K I R E Y I D Q T E Q Q K V V A A N A I E E L Y Q K K T A L E I D L S E K K D A Y E Y S

Predicted coiled coil domain
PSTPIP 148 C R D A D D A E Q A F E R V S A N G H Q K Q V E K S Q N K A K Q C K E S A T E A E R V Y R Q N I E Q
cdc15 141 C N K L N - - - S Y M R Q T K K M T G R E L D K Y N L K I R Q A A L A V K K M D A E Y R E T N E L

PSTPIP 198 L E R A R T E W E Q E H R T T C E A F Q L Q E F D R L T I L R N A L W V H C N Q L S M Q C V K D D E
cdc15 187 L L T V T R E W I D R W T E V C D A F O H I E E Y R L E F L K T N M W A Y A N I I S T A C V K D D E

PSTPIP 248 L Y E E V R L T L E G C D V E G D I N G F I Q S K S T G R E P P A P V P Y Q N Y Y - - - - -
cdc15 237 S C E K I R L T L E N T N I D E D I T O M I Q N E G T G T T I P L P E F N D Y F K E N G L N Y D I

cdc15 287 D Q L I S K A P S Y P Y S S S R P S A S A S L A S S P T R S A F R P K T S E T V S S E V V S S P P T

cdc15 337 S P L H S P V K P V S N E Q V E Q V T E V E L S I P V P S I Q E A E S Q K P V L T G S S M R R P S V

cdc15 387 T S P T F E V A A R P L T S M D V R S S H N A E T E V Q A I P A A T D I S P E V K E G K N S E N A I

cdc15 437 T K D N D D I I L S S Q L O P T A T G S R S S R L S F S R H G H G S Q T S L G S I K R K S I M E R M

cdc15 487 G R P T S P F M G S S F S N M G S R S T S P T K E G F A S N Q H A T G A S V Q S D E L E D I D P R A

cdc15 537 N V V L N V G P N M L S V G E A P V E S T S K E E D K D V P D P I A N A M A E L S S S M R R R Q S T

cdc15 587 S V D D E A P V S L S K T S S S T R L N G L G Y H S R N T S I A S D I D G V P K K S T L G A P P A A

cdc15 637 H T S A Q M Q R M S N S F A S Q T K Q V F G E Q R T E N S A R E S L R H S R S N M S R S P S P M L S

cdc15 687 R R S S T L R P S F E R S A S S L S V R Q S D V V S P A P S T R A R G Q S V S G Q Q R P S S S M S L

PSTPIP 289 - - - - - D R E V T P L I G S
cdc15 737 Y G E Y N K S Q P Q L S M Q R S V S P N P L G P N R R S S S V L Q S Q K S T S S N T S N R N N G G Y

PSTPIP 299 P S I Q P S C G V I K R F S G L L H G S P K T T P S A P A A S T E T L T P T P E R N E L V Y A S I E
cdc15 787 S G S R P S S E M G H R Y - G S M S G R S M R Q V S Q R S T S R A R S P E P T N R N S V Q S K N V D

SH3 domain
PSTPIP 349 V O A T Q G N L N S S A Q D Y - R A L Y D Y T A Q N S D E L D I S A G D I L A V I L E G E D G W W T
cdc15 836 P R A T F T A E G E P I L G Y V I A L Y D Y Q A Q I P E E I S F Q K G D T L M V L R T Q E D G W W D

PSTPIP 398 V E - - - R N G Q R G F V P G S Y L E K L
cdc15 886 G E I I N V P N S K R G L F P S N F V Q T V

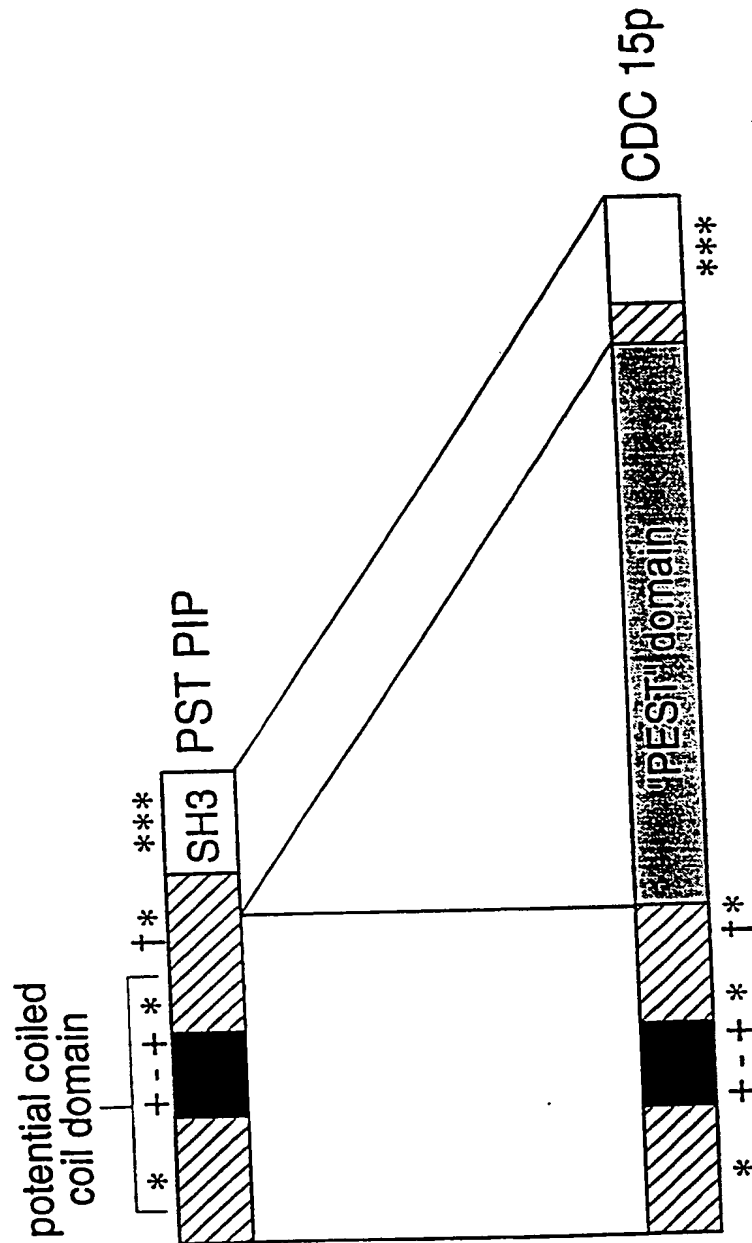
663050-423000

668050 2289000

FIG. 1B

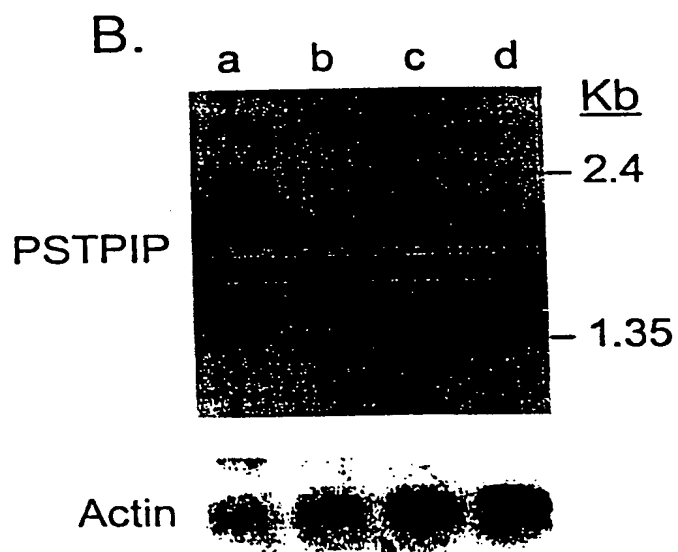
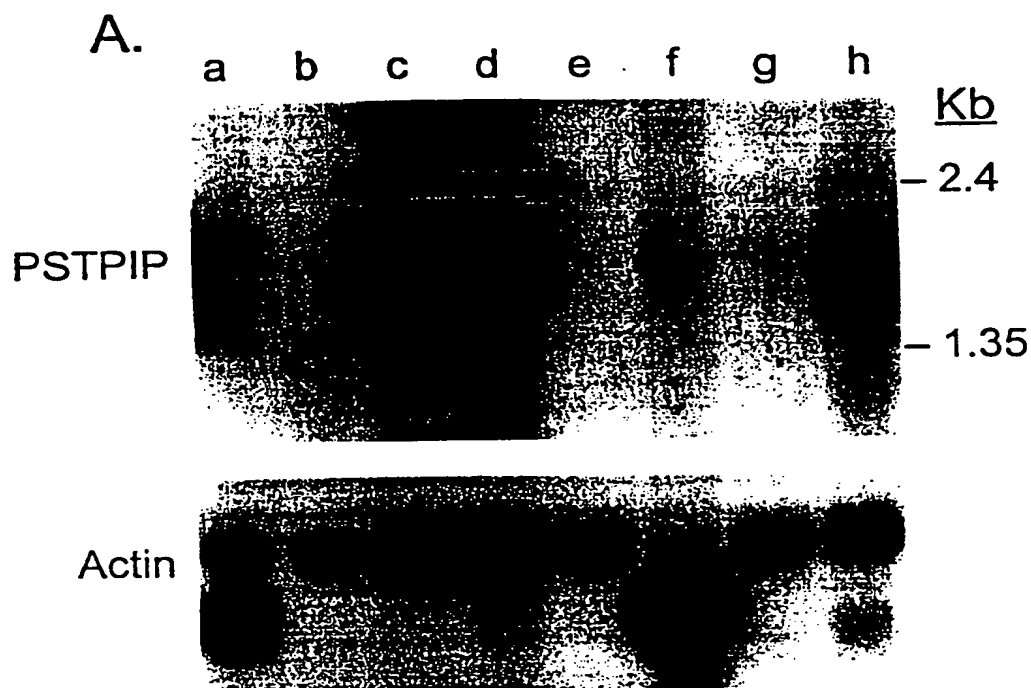
3	ps/pip.sh3	1	L	Y	D	Y	T	A	Q	N	S	D	E	L	I	S	A	G	D	I	L	A	V	I	L	E	G	E	D	G	W	W	I	V	E	R	N	G	R	G	F	V	P	G	S	Y	L	E	K	L		
4	myosin.sh3	1	L	Y	Q	Y	I	G	Q	D	V	D	E	L	S	F	N	V	N	E	V	I	E	I	L	I	E	D	S	S	G	W	W	K	G	R	L	H	G	Q	E	G	L	F	P	G	N	Y	V	E	K	I
5	spectrin.sh3	1	L	Y	D	Y	Q	E	K	S	P	R	E	V	T	M	K	K	G	D	I	L	T	L	L	N	S	T	N	K	D	W	W	K	V	E	V	N	D	R	Q	G	F	V	P	A	Y	V	K	K	L	
6	fodrin.sh3	1	L	Y	D	Y	Q	E	K	S	P	R	E	V	T	M	K	K	G	D	I	L	T	L	L	N	S	T	N	K	D	W	W	K	V	E	V	N	D	R	Q	G	F	V	P	A	Y	V	K	K	L	
7	hsp.sh3	1	L	Y	D	Y	Q	G	E	G	S	D	E	L	S	F	D	P	D	I	I	T	D	I	L	L	I	E	M	V	D	E	G	W	W	R	G	Q	C	R	G	H	F	G	L	F	P	A	Y	V	K	L
8	contactin.sh3	1	L	Y	D	Y	Q	A	G	D	C	E	I	S	F	D	P	D	I	I	T	N	I	E	M	I	D	D	G	W	W	R	G	V	C	K	G	R	Y	G	L	F	P	A	Y	V	E	.	.			

FIG. 1C



† = Conserved potential SH3 binding site (PXXP)
* = Conserved tyrosine residues

FIG. 2



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FIG. 3

a b c d e f g h i

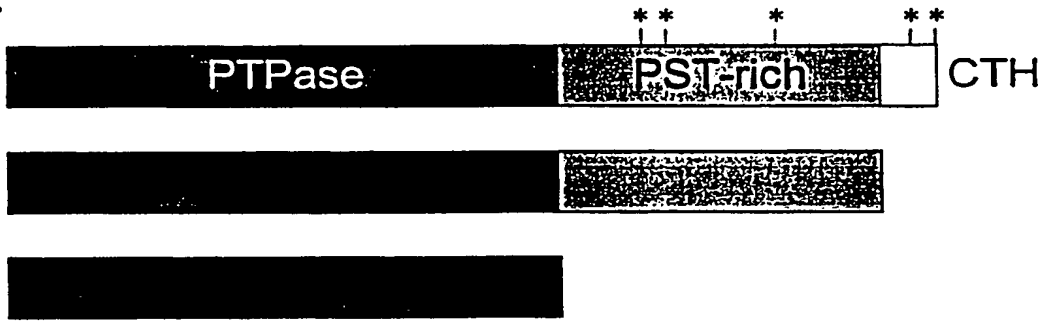


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FIG. 4

A.



CTH : C-Terminal Homology

* : PXXP

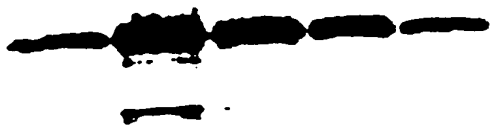
B.

a b c d e f g h i



C.

a b c d e f g h i j



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FIG. 4

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D.

$\mu\text{g peptide}$

0 2 5 10 20 40 80

PTP HSCF
 Peptide



PTP PEST
 Peptide



PTP PEP
 Peptide

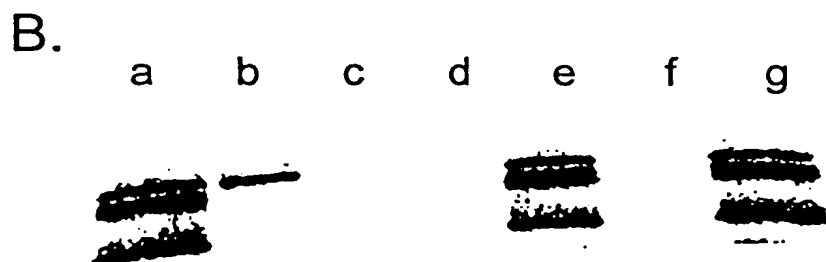
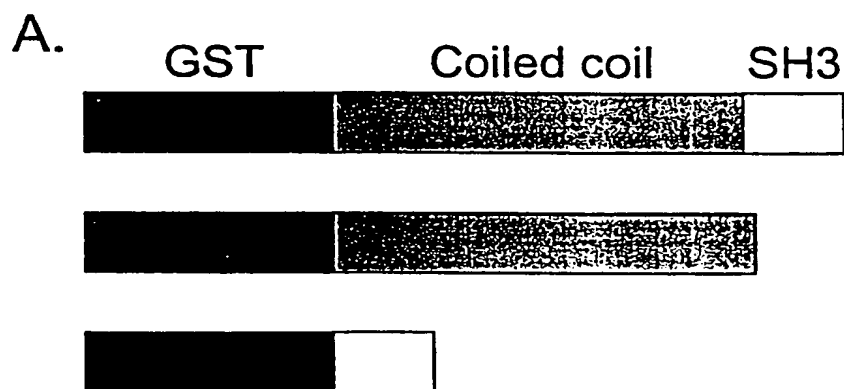


PTP HSCF
 Control Peptide



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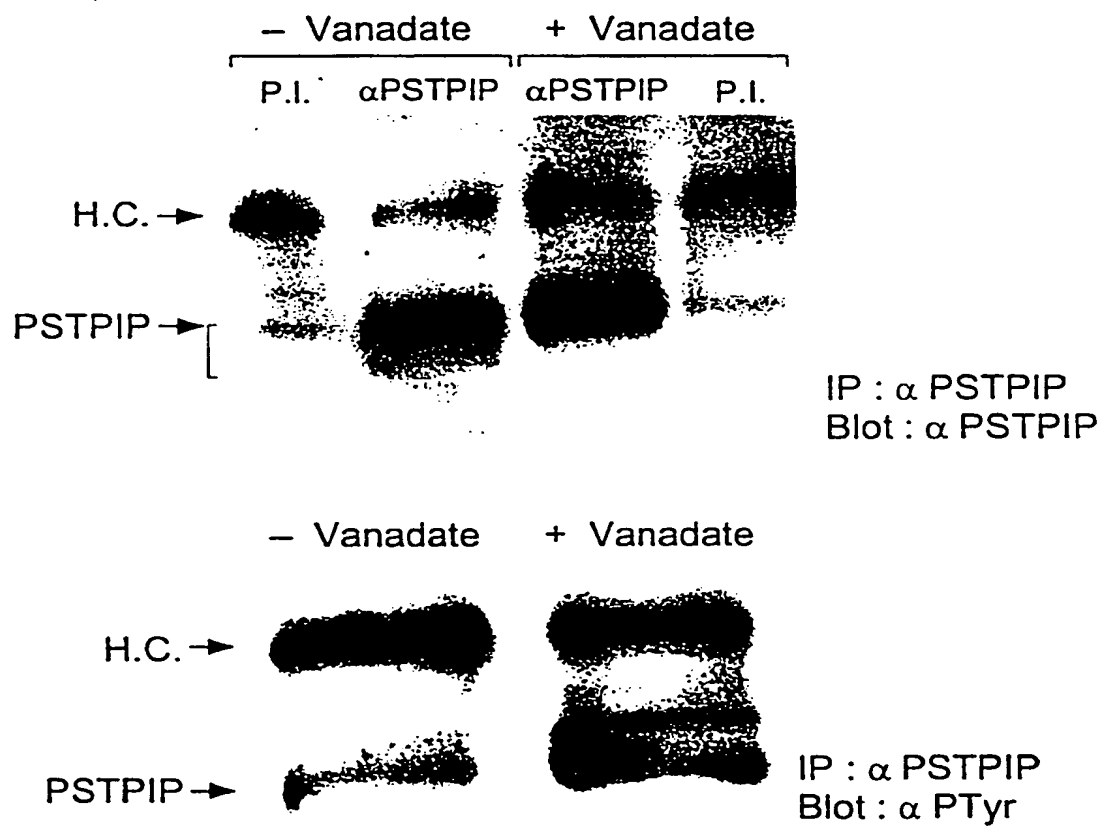
FIG. 5



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FIG. 6

A.



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FLK 6 (cont')

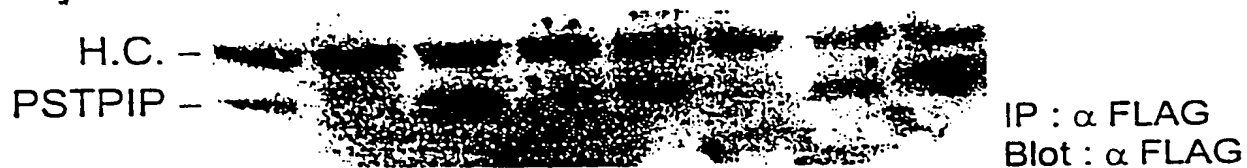
B.

PSTPIP	+	+	+	+	+	+	+	+
V-SRC	-	+	-	+	-	+	-	+
wt HSCF	-	-	-	-	-	-	+	+
C-S HSCF	-	-	+	+	-	-	-	-
D-A HSCF	-	-	-	-	+	+	-	-

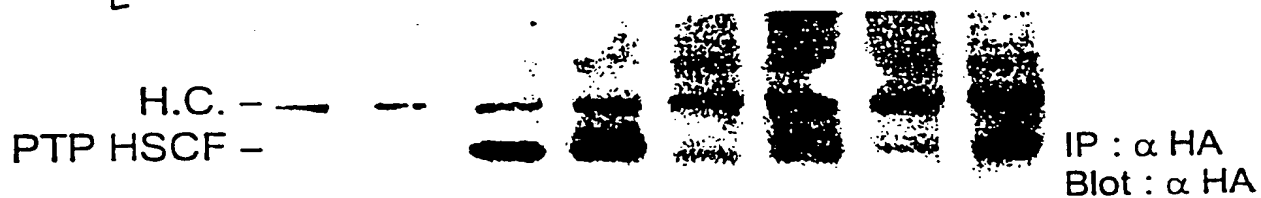
C.



D.



E



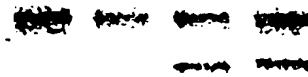
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FIG. 6 (cont.)

F.

DA HSCF	+	-	+	-
wt HSCF	-	+	-	+
PSTPIP	-	-	+	+

PTP HSCF →



IP : α FLAG
 Blot : α HA

PTP HSCF →



IP : α HA
 Blot : α HA

PSTPIP →



IP : α FLAG
 Blot : α FLAG

PSTPIP →

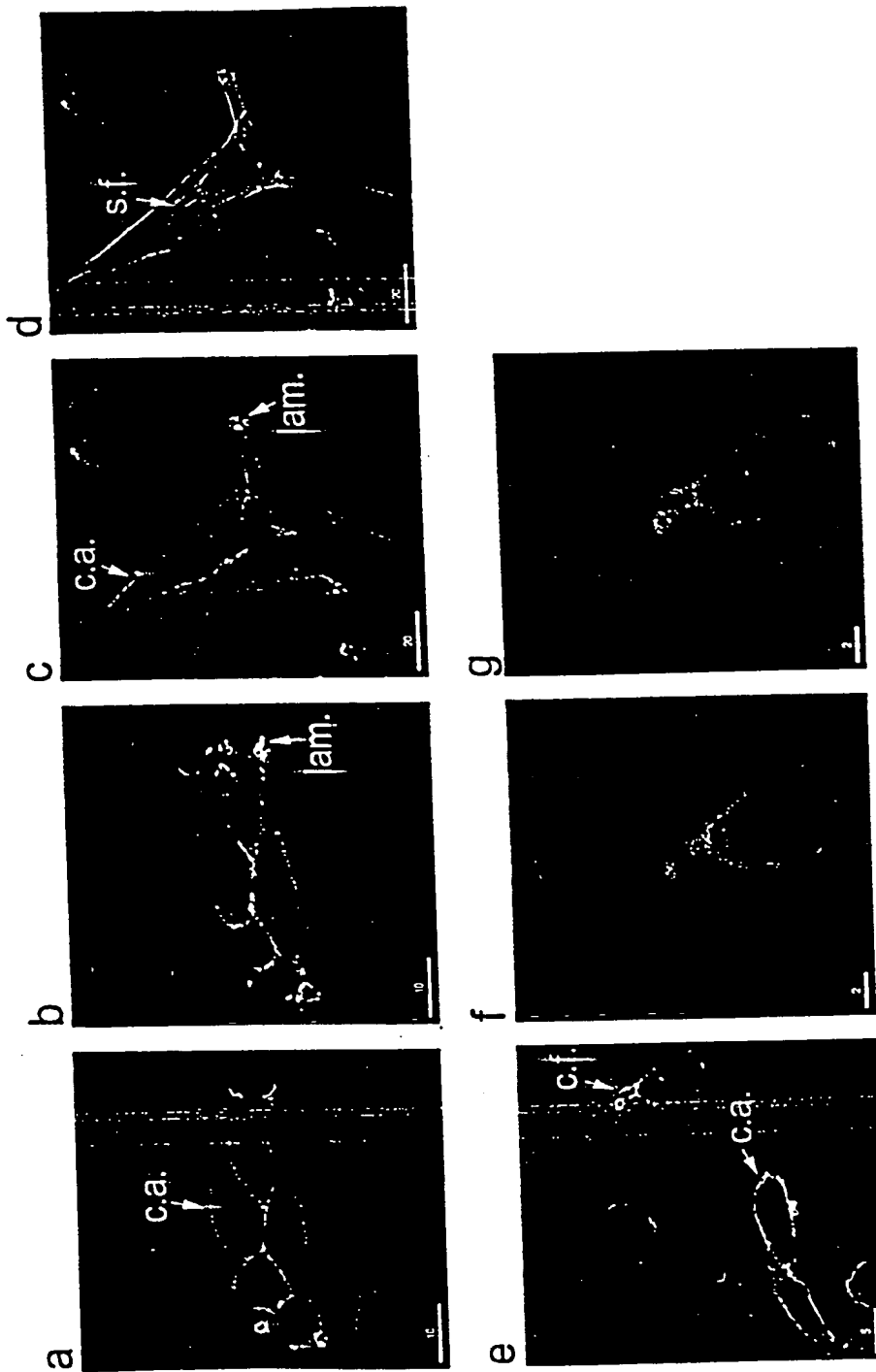


IP : α HA
 Blot : α FLAG

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Fig 7



8914

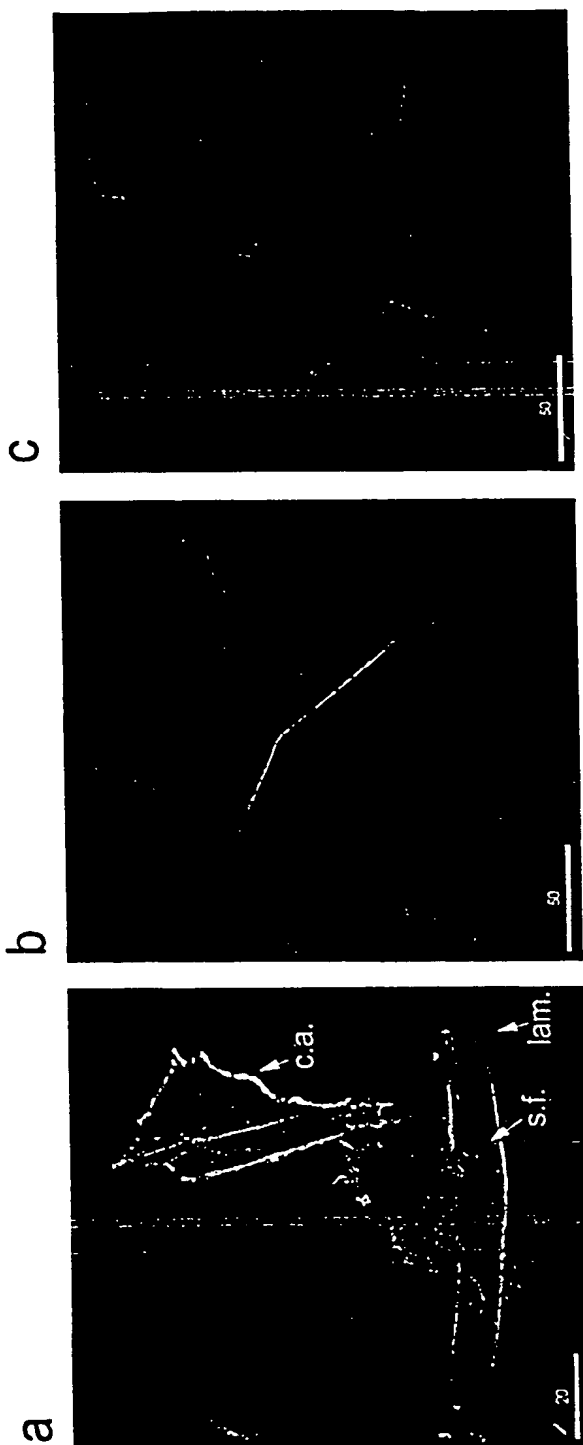


Fig 9.

F.L. $\Delta 25$ $\Delta 50$ $\Delta 75$



IP: α FLAG



IP: GST-PTP HSCF

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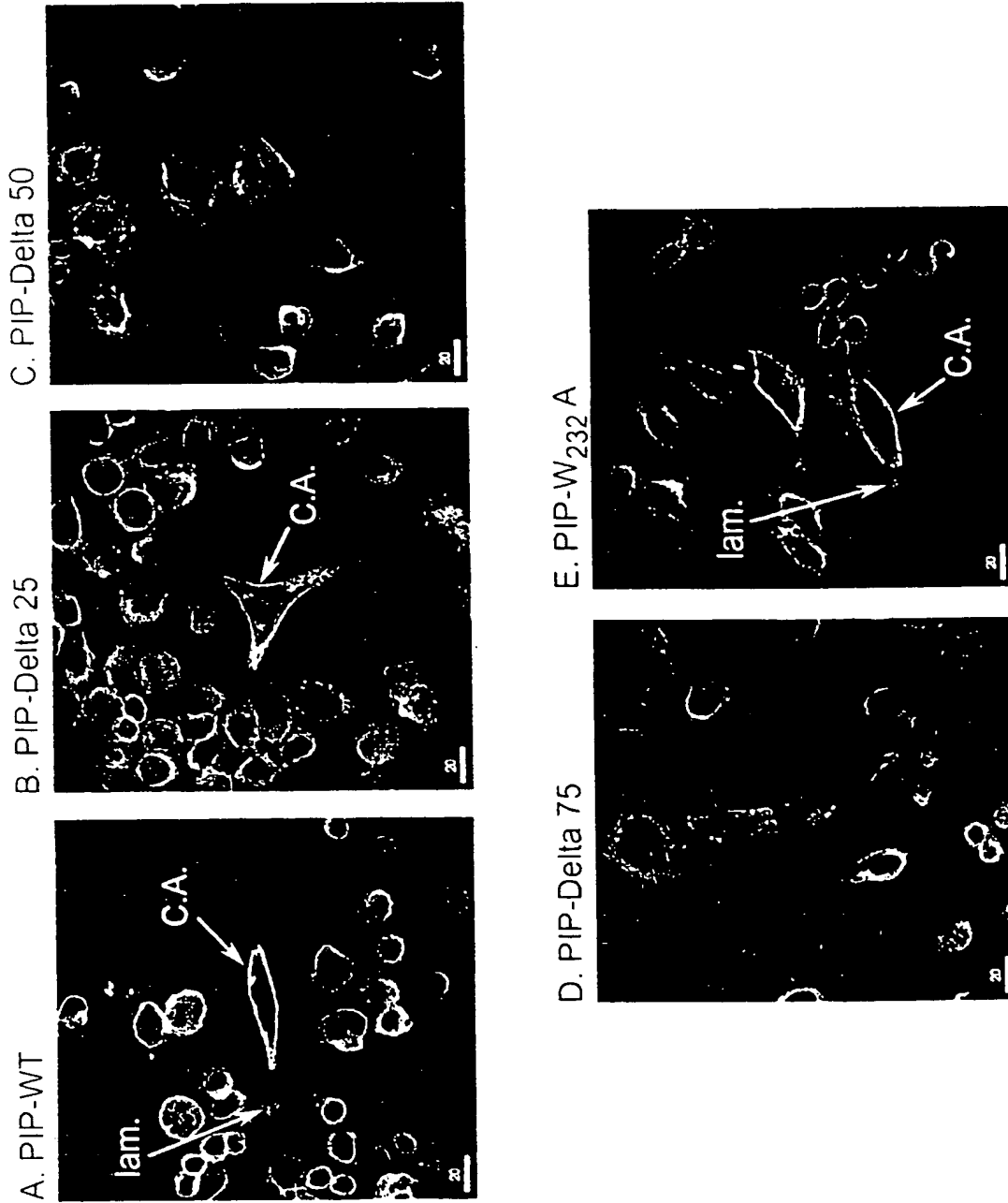


Fig 10

Fig. 4



Fig. 12

v- Src	+	+	+	+	+	+	+	+	+
WT PTP HSCF	-	+	-	+	-	+	-	+	-
C-S PTP HSCF	-	-	+	-	+	-	+	-	-
PST PIP W ₂₃₂ A	-	-	+	+	-	-	-	-	-
PST PIP WT	-	-	-	-	+	+	+	+	+
IP: α FLAG blot: α PST PIP									
IP: α HA blot: α HA									
IP: α FLAG blot: α pY									

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Fig. 13

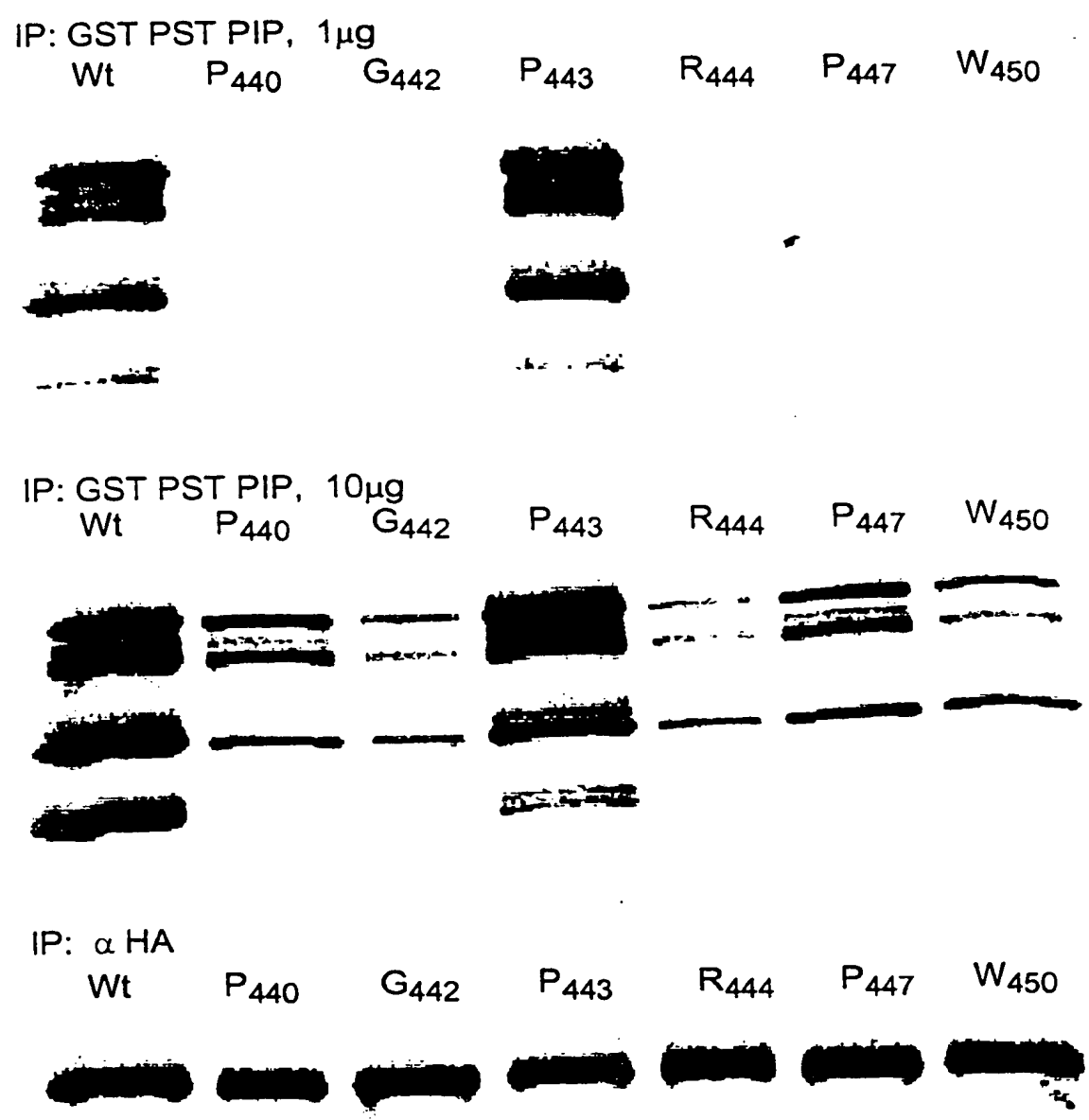
00/06 83 77

IP: GST PTP HSCF
0 Wt G432 F433 N434 L495 R436 I437 G438 R439 P440 K441 G442 P443 R444 D445 P446 P447 E449 W450

HSCF 431	L	G	F	N	L	R	I	G	R	P	K	G	P	R	D	P	P	A	E	W	T
PEP 782	-	G	F	G	N	R	F	S	K	P	K	G	P	R	N	P	P	S	A	W	-
PEST 760	I	G	F	G	N	R	C	G	K	P	K	G	P	R	D	P	P	S	E	W	T

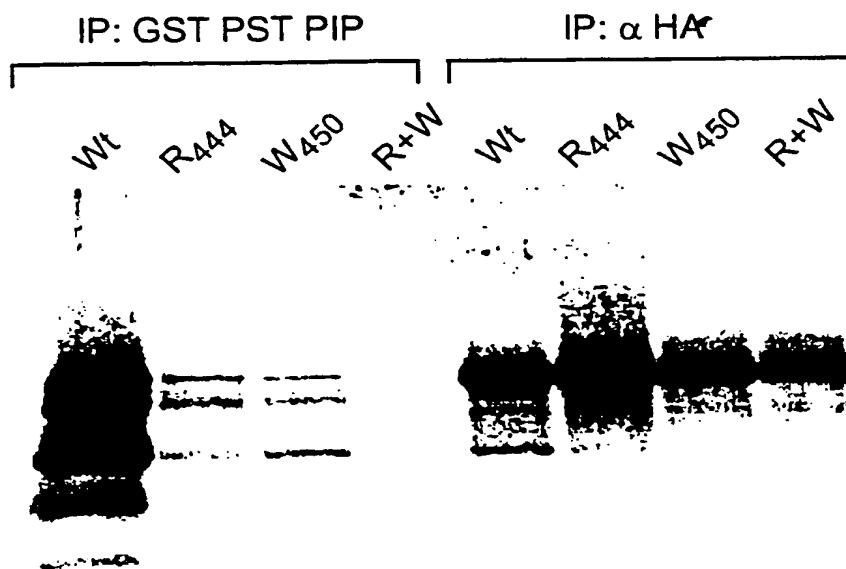
Fig. 14A/1

A.



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Fig. 14A/2



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[illegible]

4.14.1

[illegible]

IP: α FLAG
blot: α PSTPIP



IP: α Ha
blot: PST PIP



IP: α HA
blot: α HA



Fig. 15

